

## Exhibit A

WO 00/53776

PCT/CA00/00258

7/51

FIGURE 7

2221 to 2293 → ATGGCTACAGCAAGACCCCCCTGGATGTCGGTGCTCTGTGCTCTGATCACAGCCT  
 M A T A R P P W M W V L C A L I T A  
 TGCTCTGGGGTACAGGtaaccaga intron 1 tccc<sup>bg</sup> ← 2294 to  
 L L L G V T ← 4761

4762 to 5023 → AGCATGGTCTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCT  
 E H V L A N N D V S C D H P S N T V P  
 TCTGGGAGCAACCAAGGACCTGGGAGCTGGGGCCGGGAAGACGCCCGTCGGAT  
 S G S N Q D L G A G A G E D A R S D  
 GACAGCAGCAGCGCATCATCAATGGATCCGACTGCCATATGCACACCCAGCCGT  
 D S S S R I I N G S D C D M H T Q P  
 GGCAGGGCGCGCTGTGCTAAGGCCCACCAAGAGCTCTACTGCGGGCGGTGTTGGT  
 W Q A A L L L R P N Q L Y C G A V L V  
 GCATCCACAGTGGCTGCTCACGGCCGCCACTGCAGGAAGA<sup>tgatggaa</sup> ← 5024  
 H P Q W L L T A A H C R K N ← 5762

5763 to 6019 → intron 2 tcttcctc<sup>tg</sup> AGTTTTCAGAGTCCGTCT  
 V F R V R L  
 CGGCCACTACTCCCTGTCAACCAGTTATGAATCTGGGCAGCAGATGTTCCAGGGG  
 G H Y S L S P V Y E S G Q Q M F Q G  
 GTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCTAACGACCTCAT  
 V K S I P H P G Y S H P G H S N D L M  
 GCTCATCAAACGAACAGAAGAATTCTGCTCCACTAAAGATGTCAGACCCATCAAC  
 L I K L N R R I R P T K D V R P I N  
 GTCTCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGAC  
 V S S H C P S A G T K C L V S G W G T  
 AACCAAGAGCCCCCAAG<sup>tgatggatggccagg</sup> intron 3 tgac<sup>tg</sup> ← 6020 to  
 T K S P Q ← 6104  
 TGCACTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAG  
 V H F P K V L Q C L N I S V L S Q K R  
 GTGGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGAC  
 C E D A Y P R Q I D D T M F C A G D  
 AAAGCAGGTAGAGACTCCGTGCCAG<sup>tgatggatggaccc</sup> intron 4 ← 6105-6238  
 bg  
 K A G R D S C Q  
 GGTGATTCTGGGGGGCCGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCCT  
 G D A G G P V V C N G S L Q G L V S  
 GGGGAGATTACCCCTGTGCCCCGCCAACAGACCCGGGTGCTACACGAACCTCTG  
 W G D Y P C A R P N R P G V Y T N L C  
 CAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCACTCOT<sup>GAGTCATCC</sup> ← 6239 to  
 11091  
 K F T K W I Q E T I O A N S  
 GGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGAGACTCCCTT  
 CAGACCCCTCATCCCTCCAGAGATGTTGAGAATGTTGATCTCTCAGGCCCTGAC  
 CCCATGTCTCTGGACTCAGGGCTGCTTCCCCCACATGGGCTGACCGTGTCTCT  
 CTAGTTGAACCTGGGAACAATITCAAATGTCACAGGGCCGGGGGTTGCGTCTC  
 AATCTCCCTGGGGCACTTTCATCCCTCAAGCTCAGGGCCACATCCCTCTGCGAGCT  
 CTGACCCCAATTTAGTCCCAAGAATAAAACTGAGAAG